CLAIMS

1. A method for detecting the elements constituting a microorganism flora, at least some of the elements of which have an operon in common, characterized in that:

a) the genomic DNA of said flora or the mRNAs is (are) prepared,

b) at least some of the noncoding intergenic sequences located in the operon conserved in at least some of the elements of the flora are amplified, and

c) the various intergenic sequences amplified are identified in order to determine the elements of said flora.

2. The method as claimed in claim 1, characterized in that the identification of the amplified sequences is carried out on a DNA kit comprising sequences complementary to the sequences liable to be amplified from the known elements of said flora, and the demonstration of possible hybridizations making it possible to identify the elements present in the flora.

3. The method as claimed in either of claims 1 and 2, characterized in that the primers intended to amplify the intergenic sequence are located in the coding sequences of the flanking genes.

4. The method as claimed in one of claims 1 to 3, characterized in that the flora is a bacterial flora, and in that the operon is an rpoBC operon.

5. The method as claimed in claim 4, characterized in that the intergenic sequences at least partially amplified are the IGR region between the rpoB and rpoC genes (or homologous genes).

6. The method as claimed in one of claims 3 to 5, characterized in that at least one primer is chosen from the sequences SEQ ID No. 1 to SEQ ID No. 31.

7. The method as claimed in one of claims 1 to 3, characterized in that the flora is a bacterial flora, and then that the operon is a GroESL operon.

8. The method as claimed in claim 7, characterized in that the intergenic sequences at least partially

amplified are the IGR region between the GroES and GroEL genes (or homologous genes).

9. The method as claimed in one of claims 3, 7 and 8, characterized in that at least one primer is chosen from the sequences SEQ ID No. 32 to SEQ ID No. 52.

10. A DNA chip, characterized in that it has, at its surface, sequences complementary to the noncoding intergenic sequences located in an operon which is conserved between various species.

11. The DNA chip as claimed in claim 10, characterized in that the sequences of several organisms, complementary to the noncoding intergenic sequences located in said conserved operon, are present at the surface of said chip.

12. A diagnostic kit for carrying out a method as claimed in one of claims 1 to 9, characterized in that it contains degenerate primers for amplifying one or more intergenic regions of an operon which is conserved among species and, optionally, a DNA chip as claimed in either of claims 10 and 11.

13. A primer for carrying out a method as claimed in one of claims 1 to 9, characterized in that it is chosen from the sequences SEQ ID No. 1 to SEQ ID No. 52.

14. A genomic sequence of a microorganism, characterized in that it can be obtained by amplification with a pair of primers chosen from:

- (a sequence chosen from the sequences SEQ ID No. 1 to SEQ ID No. 8)/(a sequence chosen from the sequences SEQ ID No. 9 to SEQ ID No. 11),
- (a sequence chosen from the sequences SEQ ID No. 12 to SEQ ID No. 15)/(a sequence chosen from the sequences SEQ ID No. 16 to SEQ ID No. 31),
- SEQ ID No. 32/ SEQ ID No. 33,
- (SEQ ID No. 34, SEQ ID No. 35 or SEQ ID No. 39)/(a sequence chosen from the sequences SEQ ID No. 36 to SEQ ID No. 38 or SEQ ID No. 40 to SEQ ID No. 52 or SEQ ID No. 139),
- (a sequence chosen from the sequences SEQ ID No. 53, SEQ ID No. 55 to SEQ ID No. 58)/(a sequence chosen from the sequences SEQ ID No. 54, SEQ ID No. 59 to SEQ ID No. 61).

15. The genomic sequence as claimed in claim 14, characterized in that it is a sequence chosen from SEQ ID No. 63 to SEQ ID No. 138 and SEQ ID No. 140 to SEQ ID No. 189.

16. The DNA chip as claimed in claim 10 or 11, having, at its surface, a plurality of oligonucleotides comprising fragments more than 30 bases long, chosen from the fragments of the sequences SEQ ID No. 63 to SEQ ID No. 138 and SEQ ID No. 140 to SEQ ID No. 189.